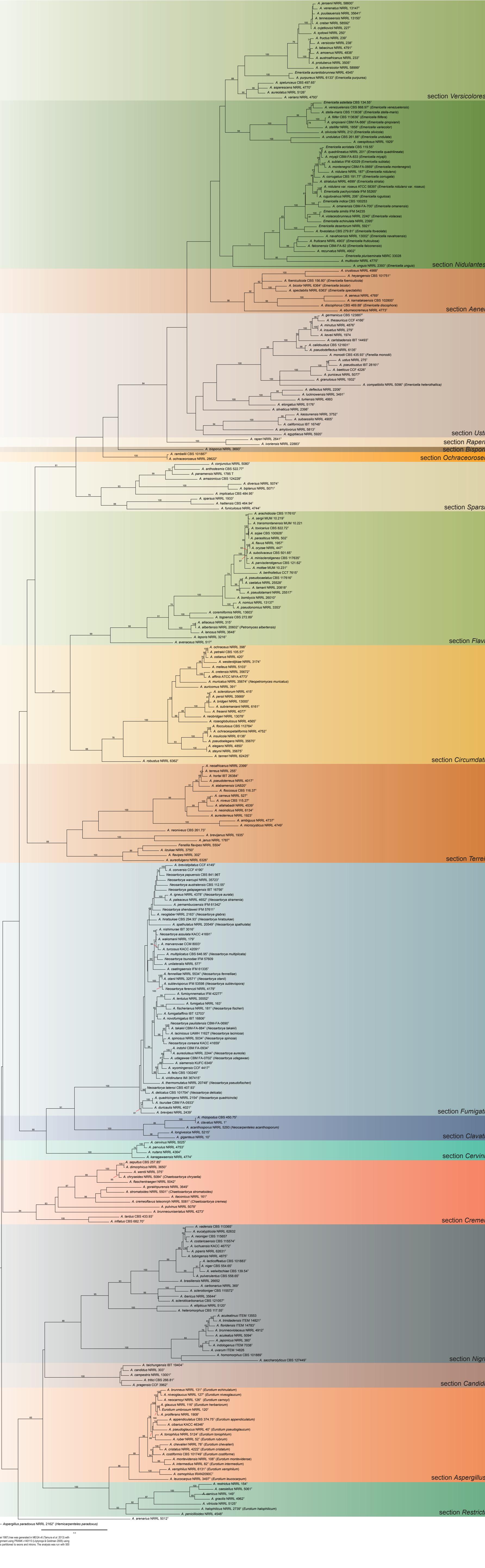


section Versicolores



Aspergillus paradoxus NRRL 2162 (*Hemicarpenteles paradoxus*)

Supp. Fig. 2. An initial alignment of calmodulin sequences was made using MFFT (27 Feb 2010) with the -NCG option (Saitou & Saito 1978). Upon the aligned sequences, a Neighbor-Joining (Saitou & Nei 1978) tree was generated in BioEdit (Hallsworth et al. 2010) with the -T option (Hallsworth et al. 2010). The tree then served as a guide tree in the second alignment using PRANK (V14110; Lipshutz & Godwin 2005) using the -F option. A phylogenetic reconstruction was conducted using Maximum Likelihood analysis in raxML v3.1 using the GTR+T model (Silvestri & Michalek 2011). The partial calmodulin dataset was partitioned to peers and introns. The analysis was run with 500 bootstraps replicates.

Kumar S (1983). A new method for estimating evolutionary rate of base substitutions through comparative studies of nucleic acid sequences. *Journal of Molecular Evolution* 18: 111–120.

Lipshutz A, Godwin D (2005). An algorithm for progressive multiple alignment of sequences with insertions. *Proceedings of the National Academy of Sciences of the United States of America* 102: 10551–10562.

Silvestri D, Michalek D (2011). RaxML: a graphical front-end for RAxML. *Organisms Diversity & Evolution* 12: 335–337.

Calmodulin

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